

**Query= SEQ ID NO:1**  
(2772 letters)

Score E  
(bits) Value

Sequences producing significant alignments:

AL365232.24.1.120846	<u>1913</u>	0.0
AL445569.1.1.47057	<u>733</u>	0.0
AL360236.26.1.154998	<u>355</u>	1e-94

>AL365232.24.1.120846  
Length = 120846

Score = 1913 bits (965), Expect = 0.0

Identities = 965/965 (100%)

Strand = Plus / Plus

Query: 1808 aggtacagtccatagaatccaagctggactgcctactagacatctatcaacaggccttc 1867  
|||||||  
Sbjct: 61339 aggtacagtccatagaatccaagctggactgcctactagacatctatcaacaggccttc 61398

Query: 1868 ggaaaggctctgcctcagccctcgcttggcttcatccagatcccacctttgaatgtg 1927  
|||||||  
Sbjct: 61399 ggaaaggctctgcctcagccctcgcttggcttcatccagatcccacctttgaatgtg 61458

Query: 1928 aacagacatctgactatcaaagccctgtggatagcaaagatcttcgggttccgcacaaa 1987  
|||||||  
Sbjct: 61459 aacagacatctgactatcaaagccctgtggatagcaaagatcttcgggttccgcacaaa 61518

Query: 1988 acagtggctgcttatccagatcaacttagtgccaaacatctcgagaggcctgcagttcattc 2047  
|||||||  
Sbjct: 61519 acagtggctgcttatccagatcaacttagtgccaaacatctcgagaggcctgcagttcattc 61578

Query: 2048 tgacccaaatgagttcagtgccagactttctacgcgcttagccctactatgcacagtc 2107  
|||||||  
Sbjct: 61579 tgacccaaatgagttcagtgccagactttctacgcgcttagccctactatgcacagtc 61638

Query: 2108 aagcaacacaggtgccaattagtcaaagcgatggctcagcagtggcagccaccaacacca 2167  
|||||||  
Sbjct: 61639 aagcaacacaggtgccaattagtcaaagcgatggctcagcagtggcagccaccaacacca 61698

Query: 2168 ttgcaaaccataatacggcaccaagccagcagccccacaactttacagatccac 2227  
|||||||  
Sbjct: 61699 ttgcaaaccataatacggcaccaagccagcagccccacaactttacagatccac 61758

Query: 2228 ctcctctcccagccatcaagcatctgccaggccagaaactctgcaccttaaccctgcag 2287  
|||||||  
Sbjct: 61759 ctcctctcccagccatcaagcatctgccaggccagaaactctgcaccttaaccctgcag 61818

Query: 2288 gcttacaggaaagcattctgacgtcaccacctgccttgcctccaaggaaaatgttc 2347  
Sbjct: 61819 gcttacaggaaagcattctgacgtcaccacctgccttgcctccaaggaaaatgttc 61878

Query: 2348 agttgcacagtcaaattctaccaaggaccgttatgagggaaaagcttgacatggag 2407  
Sbjct: 61879 agttgcacagtcaaattctaccaaggaccgttatgagggaaaagcttgacatggag 61938

Query: 2408 gagaaactctgttgtctgtcccattgggccgaaggacttggcaatcttgc 2467  
Sbjct: 61939 gagaaactctgttgtctgtcccattgggccgaaggacttggcaatcttgc 61998

Query: 2468 tgcaaaacctgatcaggtcgaccgaggaactgaatacataactttcaggagtgactcaa 2527  
Sbjct: 61999 tgcaaaacctgatcaggtcgaccgaggaactgaatacataactttcaggagtgactcaa 62058

Query: 2528 gtggctccagaggcagccaaagatttacccaaatggagggaaatccaaattgttataa 2587  
Sbjct: 62059 gtggctccagaggcagccaaagatttacccaaatggagggaaatccaaattgttataa 62118

Query: 2588 ctgatgaagaggtggtcccgaagagacagacagacactttgatgccgcaccgcagc 2647  
Sbjct: 62119 ctgatgaagaggtggtcccgaagagacagacagacactttgatgccgcaccgcagc 62178

Query: 2648 ctgccaggaaagctgccttgcattcagactctctaaggacttgcacgtcatctc 2707  
Sbjct: 62179 ctgccaggaaagctgccttgcattcagactctctaaggacttgcacgtcatctc 62238

Query: 2708 agagcattttaaggcaggagaaagtacagatgcctcagttgcctcatgtcaaactga 2767  
Sbjct: 62239 agagcattttaaggcaggagaaagtacagatgcctcagttgcctcatgtcaaactga 62298

Query: 2768 aataa 2772  
Sbjct: 62299 aataa 62303

Score = 438 bits (221), Expect = e-120  
Identities = 221/221 (100%)  
Strand = Plus / Plus

Query: 1221 tcagaagctaagtttaaggagcgagtgcgcattggctagccccagggccagagtattaa 1280  
Sbjct: 310 tcagaagctaagtttaaggagcgagtgcgcattggctagccccagggccagagtattaa 369

Query: 1281 gagccgacaagcctcagtaggtacaggaggtccccaaagcaccgacatcacagccgaggg 1340  
Sbjct: 370 gagccgacaagcctcagtaggtacaggaggtccccaaagcaccgacatcacagccgaggg 429

Query: 1341 cagtcccaccaaagtgcagaagagctggagcttcaacgaccgaacccgcttcggccctc 1400  
Sbjct: 430 cagtcccaccaaagtgcagaagagctggagcttcaacgaccgaacccgcttcggccctc 489

Query: 1401 gctgcgcctcaaaagttctcagccaaaaccagtatagatg 1441  
Sbjct: 490 gctgcgcctcaaaagttctcagccaaaaccagtatagatg 530

Score = 268 bits (135), Expect = 2e-68  
Identities = 135/135 (100%)  
Strand = Plus / Plus

Query: 1548 cagaattatgaaatttcatgttgcacaaacggaaagtttaaggaaacattacgtccatata 1607  
Sbjct: 57459 cagaattatgaaatttcatgttgcacaaacggaaagtttaaggaaacattacgtccatata 57518

Query: 1608 tgtaaaagatgtcattgaacaatattctgtggcatctggacatgttgtttagattaa 1667  
Sbjct: 57519 tgtaaaagatgtcattgaacaatattctgtggcatctggacatgttgtttagattaa 57578

Query: 1668 aagccttcaaacacg 1682  
Sbjct: 57579 aagccttcaaacacg 57593

Score = 264 bits (133), Expect = 3e-67  
Identities = 133/133 (100%)  
Strand = Plus / Plus

Query: 1682 gtgttgcataattttggaaaaggccaaatcacatcagataagaagagccgagaaaaaa 1741  
Sbjct: 59453 gtgttgcataattttggaaaaggccaaatcacatcagataagaagagccgagaaaaaa 59512

Query: 1742 taacagcagaacatgagaccacagacgatctcagttatgtctcggtcggtggtaaggttg 1801  
Sbjct: 59513 taacagcagaacatgagaccacagacgatctcagttatgtctcggtcggtggtaaggttg 59572

Query: 1802 aaaaacaggtaca 1814  
Sbjct: 59573 aaaaacaggtaca 59585

Score = 218 bits (110), Expect = 1e-53  
Identities = 110/110 (100%)  
Strand = Plus / Plus

```
Query: 1441 gctgacacagcccttggcactgtatgtatgtatgtaaaaaggatgccagtgtatgtta 1500
          ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 36634 gctgacacagcccttggcactgtatgtatgtatgtaaaaaggatgccagtgtatgtta 36693
```

Query: 1501 tcagtggaaagacctccccccaccactaaaactgtcattcgagctatcatg 1550  
||| ||| ||| ||| ||| ||| |||  
Sbjct: 36694 tcagtggaaagacctccccccaccactaaaactgtcattcgagctatcatg 36743

>AL445569.1.1.47057  
Length = 47057

Score = 733 bits (370), Expect = 0.0  
Identities = 394/401 (98%), Gaps = 6/401 (1%)  
Strand = Plus / Plus

Query: 1 atgccccggccaccacgcggaggagaggagggcgccgcccggctctgggtgaagagc 60  
||| ||| ||| ||| ||| |||  
Sbjct: 4316 atgccccggccaccacgcggaggagaggagggcgccgcccggctctgggtgaagagc 4375

Query: 61 ggcgca...gtggag 120  
Sbjct: 4376 ggcgca...gtggag 4435

Query: 121 tcggggccggggcagggtgctgctgaactcggcagccgccaggggcgacggcctgtactg 180  
Sbjct: 4436 tccggggccggggcagggtgctgctgaactcggcagccgccaggggcgacggcctgtactg 4495

Query: 181 ctgggcacccgcgcggcacgctcggtggcggcggcggctgaggagagccgcgg 240  
|||||||  
Sbjct: 4496 ctgggcacccgcgcggcacgctcggtggcggcggcggctgaggagagccgcgg 4555

Query: 301 agctgccggcgcaacgtcaagtaccggcgggtgcagaactaccgtacaacgtgctggag 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 4616 agactaccqacgcacacgtcaagtaccqacgggtgcagaactaccgtacaacgtgctggag 4675

Query: 361 agaccccgccggctgggcgttcatctaccacgcttcgt 398  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 4676 agaccccgccggctgggcgttcatctaccacgcttcgt 4713

>AL360236.26.1.154998  
Length = 154998

Score = 355 bits (179), Expect = 1e-94  
Identities = 179/179 (100%)  
Strand = Plus / Plus

Query: 615 agataaccattgttcttatcgcttcaatagcagttgttctgcaaaaactcaggtaatat 674  
Sbjct: 99107 agataaccattgttcttatcgcttcaatagcagttgttctgcaaaaactcaggtaatat 99166

Query: 675 ttttgcacgtctgcactcagaagtctccgttccctacagatcctccgcatggtgcat 734  
Sbjct: 99167 ttttgcacgtctgcactcagaagtctccgttccctacagatcctccgcatggtgcat 99226

Query: 735 ggaccgaaggggaggcacttgaaattactgggttcagtggttatgctcacagcaagg 793  
Sbjct: 99227 ggaccgaaggggaggcacttgaaattactgggttcagtggttatgctcacagcaagg 99285

Score = 254 bits (128), Expect = 3e-64  
Identities = 128/128 (100%)  
Strand = Plus / Plus

Query: 489 ggagttcgtgatgtcgattgtcgctttgggttggagttcatcattcgaaatctggctgcggg 548  
Sbjct: 63722 ggagttcgtgatgtcgattgtcgctttgggttggagttcatcattcgaaatctggctgcggg 63781

Query: 549 ttgctgttgcatacatagaggatggcaaggaagactgaggttgctcgaaagccctctg 608  
Sbjct: 63782 ttgctgttgcatacatagaggatggcaaggaagactgaggttgctcgaaagccctctg 63841

Query: 609 tgttata 616  
Sbjct: 63842 tgttata 63849

Score = 254 bits (128), Expect = 3e-64  
Identities = 128/128 (100%)  
Strand = Plus / Plus

Query: 791 aggaattaatcacagcttggtacataggattttggttcttattttcgtcttcctt 850  
Sbjct: 99547 aggaattaatcacagcttggtacataggattttggttcttattttcgtcttcctt 99606

Query: 851 tctatctggtgaaaaggatgccaataaaagagtttctacatatgcagatgctctgg 910  
|||||||  
Sbjct: 99607 tctatctggtgaaaaggatgccaataaaagagtttctacatatgcagatgctctgg 99666

Query: 911 ggggcaca 918  
|||||||  
Sbjct: 99667 ggggcaca 99674

Score = 222 bits (112), Expect = 9e-55  
Identities = 112/112 (100%)  
Strand = Plus / Plus

Query: 919 attacattgacaactattggctatggagacaaaactccctaacttgctggaaagattg 978  
|||||||  
Sbjct: 127044 attacattgacaactattggctatggagacaaaactccctaacttgctggaaagattg 127103

Query: 979 ctttctgcaggcttgcactccttgcatttcatttgcacttcctgccg 1030  
|||||||  
Sbjct: 127104 ctttctgcaggcttgcactccttgcatttcatttgcacttcctgccg 127155

Score = 194 bits (98), Expect = 2e-46  
Identities = 98/98 (100%)  
Strand = Plus / Plus

Query: 1123 cagtgtttggcgtagttacgcagctgatgagaaatctgtttcattgcaacctgg 1182  
|||||||  
Sbjct: 142267 cagtgtttggcgtagttacgcagctgatgagaaatctgtttcattgcaacctgg 142326

Query: 1183 ccacacttgaaggcttgcacacctgcagccctaccaa 1220  
|||||||  
Sbjct: 142327 ccacacttgaaggcttgcacacctgcagccctaccaa 142364

Score = 190 bits (96), Expect = 3e-45  
Identities = 96/96 (100%)  
Strand = Plus / Plus

Query: 1030 ggcattttggctcaggtttgcattaaagtacaagaacaacaccggcagaaacacttt 1089  
|||||||  
Sbjct: 133095 ggcattttggctcaggtttgcattaaagtacaagaacaacaccggcagaaacacttt 133154

Query: 1090 gagaaaagaaggaacccagctgccaacctcattcag 1125  
|||||||  
Sbjct: 133155 gagaaaagaaggaacccagctgccaacctcattcag 133190

Score = 182 bits (92), Expect = 8e-43  
Identities = 92/92 (100%)  
Strand = Plus / Plus

Query: 399 ttttcccttgtcttggttgcatttcgtcagtgttttaccatccctgagcacac 458  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 25695 ttttcccttgtcttggttgcatttcgtcagtgttttaccatccctgagcacac 25754

Query: 459 aaaattggcctaaggcctttgatccctgg 490  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 25755 aaaattggcctaaggcctttgatccctgg 25786



**Nucleotide**

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1: AL365232. Human DNA sequenc...[gi:13234949]

Links

LOCUS AL365232 120846 bp DNA linear PRI 01-MAR-2001

DEFINITION Human DNA sequence from clone RP11-257K9 on chromosome 6, complete sequence.

ACCESSION AL365232

VERSION AL365232.24 GI:13234949

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 120846)

AUTHORS Williams,S.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Mar 5, 2001 this sequence version replaced gi:13160293. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-257K9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-257K9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-257K9 is at 1 in this sequence. The

**NCBI**




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Display <input type="button" value="default"/>	Show: <input type="button" value="20"/> <input type="button" value="Send to"/> <input type="button" value="File"/>		<input type="button" value="Get Subsequence"/>	<input type="button" value="Features"/>

**1: AL445569. Human DNA sequenc...[gi:10862812]**

Links

**LOCUS** AL445569 47057 bp DNA linear PRI 17-OCT-2000  
**DEFINITION** Human DNA sequence from clone RP11-135M8 on chromosome 6, complete sequence.  
**ACCESSION** AL445569 AL161434  
**VERSION** AL445569.1 GI:10862812  
**KEYWORDS** HTG.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 47057)  
**AUTHORS** Bates,K.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
**COMMENT** During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>  
RP11-135M8 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>  
**VECTOR:** pBACe3.6  
**IMPORTANT:** This sequence is not the entire insert of clone RP11-135M8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
The true right end of clone RP3-474G15 is at 100 in this sequence.  
The true right end of clone RP11-135M8 is at 47057 in this sequence.



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**[1: AL360236. Human DNA sequenc...[gi:13398790]]**

Links

**LOCUS** AL360236 154998 bp DNA linear PRI 19-MAR-2001  
**DEFINITION** Human DNA sequence from clone RP11-380M3 on chromosome 6, complete sequence.  
**ACCESSION** AL360236  
**VERSION** AL360236.26 GI:13398790  
**KEYWORDS** HTG.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 154998)  
**AUTHORS** Clark,G.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
**COMMENT** On Mar 21, 2001 this sequence version replaced gi:13161652. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-380M3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6  
**IMPORTANT:** This sequence is not the entire insert of clone RP11-380M3 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-380M3 is at 1 in this sequence. The